

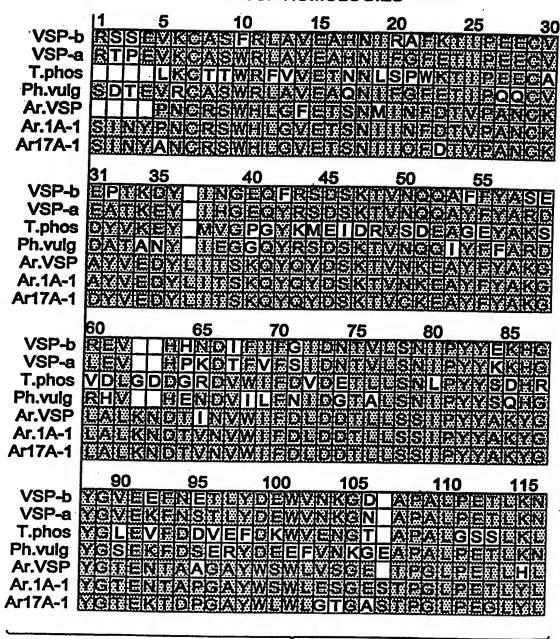
Title: Compositions and Methods for Altering Amino Acid Content of

In or(s): Rao et al.
Application No: 09/478,598

Atty Dkt No: 5718-16A (35718/193734)

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#### **VSP HOMOLOGIES**



TO FIG. 1B.

FIG. 1A.



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### FROM FIG. 1A.

بترتي

				1 17		<u></u>	<u>~.</u>						
		120		25	130		13	5		140		14	15
VSP-b	320 202	#   # S			7 競送		YL		Mr.	25XX	建三		K
VSP-a	TARREST AND ADDRESS		\[ <u>\</u> \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\			SER	ΤŁ	8					K
T.phos	X OE	VEK						RH	RS				М
Ph.vulg	YNK	EVS						8		3038	XEZ	MIL	K
Ar.VSP	X E N	EEE	<b>ES</b>			BE	WE				ğ		K
Ar.1A-1	经压风	透透医				SOR	W.K		S		¥.V/		K
Ar17A-1	X O X	111	WO!		####E	沙区	W	(4)	WK	IND	ITI	-NE	
											,		
	1	50	15	55	160			165		17	70		175
VSP-b	KAG	是镁铁	WEC	<b>1</b> { \$ \$ \$ \$ { }	FI(4 b)	## _		88 #		LE	Y	61817.	
VSP-a		X H	WEK	4( <b>28</b> 88)	KD		PS	7 5	N.	1.V.	Y	Q 8 8 6	A
T.phos	NAS	FHD	XHK		RGS		H	GK	TA	Ti	X	(SE	R
Ph.vulg	KAG	YNT	MEK		KO		NS	AE	N	VX	Y	<b>1887</b>	E
Ar.VSP			WKH	VIII				7 8 R		V.V	866	SK	V
Ar.1A-1		VIK	WKE	(###)	KEK	<b>E</b> S	KE	8 8 æ		V.V	Ye K	SK	V
Ar17A-1	MAG	YEY	W SE	[[		es	2][2	Re		W.Y	446	(SK	V
						(							
		180		185	19	0	_ 1	95		20	0	2	205
		战上段		R	£ 888			SE	<b>[</b> 8]	GC			15
	REK		ecy,	NEN		C D	<b>6</b> ) []	SB		GG			S
T.phos	RNA	MXE	EGF	RIV	SNS		<u> </u>	S		GS	SM	S	Y
	RAK	EVQ	EGX	RHY	GN	G D	@ W	ND	選K	GE	NR	AI	
Ar.VSP	RNS		eex.	NIV		SE	8	A D		ED	33.5	<b>G</b> _	
Ar.1A-1	RNS	医双环环	KER	Nativ	GNI	GEK	*		$\mathbb{R}V$	ED		G	
Ar17A-1	RNK	異なば	KGY	NEW	GNI	SIDK		A B		ED	<b>88.2</b>	9_	
1000		210			218_								
T.phos	RSE		<b>労幣党</b>										
	RISIE		N E M	asas T									
	RVF	K & K		YYV									
	<b>XXX</b>			***									

FIG. 1B.

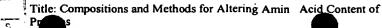


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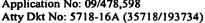
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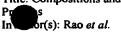
PROF	POSED	VSPB	METHI	ONINE-E	NRICHE	D VAR	IANTS	
	11	5	10	15	2	0	. 25	30
VSP	BRSE	BEVKC	ASF	RLAVE	AHNTI	RAFK	TIPE	EQV
VSPB-Met1		M			M			M
VSPB-Met2	0	M			M			M
VSPB-Met30		M			M		M	M
	04	0.5	40	45	_	^		
Vend	31	35	40	45	<u>5</u>	<u>U</u>	<u>55</u>	60
VSPA-Met10	रीह्ममा	KDYI	NGEC	FRSD	SKIUN	<u>IQQA</u>	<u> FFYA</u>	
VSPB-Met20	M	<u>M</u>		M	<del> </del>			<u>M</u>
VSPB-Met30	M	M M		<u>M</u> M_	N		<del></del> _	M
VOI PAVIEWO	IVI IVI	IVI			IV	1		M
	61	65	70	75	8		85	90
VSP	EVH	HNDI	FIFG	IDNT	ILSNI	PYY	EKHG	YGV
VSPB-Met10	M	M		M I	M			
VSPB-Met20	M	M M		M I	M			M
VSPB-Met30	M	M M			M M			M
				400		_	4.45	
Vene	91	95	100	105		0	115	120
VSPQ Mote	EEL	NETIL	Y D EW	VNKGL	JAPAL	PEI	<u>-KNYI</u>	NKL
VSPB-Met10 VSPB-Met20				3.4		<u> </u>		·
VSPB-Met30		<u>M</u>		M				
VOPD-INEWU	M	M		M		<del></del>		
	121	125	130	135	14	0	145	150
VSPB	LISL	3 FKIN	/FILS		KMAV	TEAN		AGF
VSPB-Met10	M	M			M		M	
VSPB-Met20	M	M	M	M	M		M	M
VSPB-Met30	M	M	M	M	M	_M_	M	M
	151	155	160	165	170		175	400
	HTW	100 EO I I I	KIDIP		NALS		MADEN	180
VSPB-Met10	13 1 44 1	EWLIL	- NUIP		MAILO	IKSA	M	M
VSPB-Met20			<del></del>	M	M		M	M
VSPB-Met30	<del></del>		M	MM	M		M	M
		• • • • • • • • • • • • • • • • • • • •						
	181	185	190	195	200		205	210
VSPB	<u>RQG \</u>	RIVG		DQWS D	LILG DI		SRTF	KL
VSPB-Met10			<u>M</u>			<u>M</u>		
VSPB-Met20			<u>M</u>		M	<u>M</u>	<u>M</u>	
VSPB-Met30			M		<u>M</u>	<u>M</u>	M	
	211	215 21	R					
VSPB	PNP	YYITE			****			
VSPB-Met10	M		<u></u>					
VSPB-Met20	M			· · · · · · · · · · · · · · · · · · ·				
VSPB-Met30	M						-	

FIG. 2.



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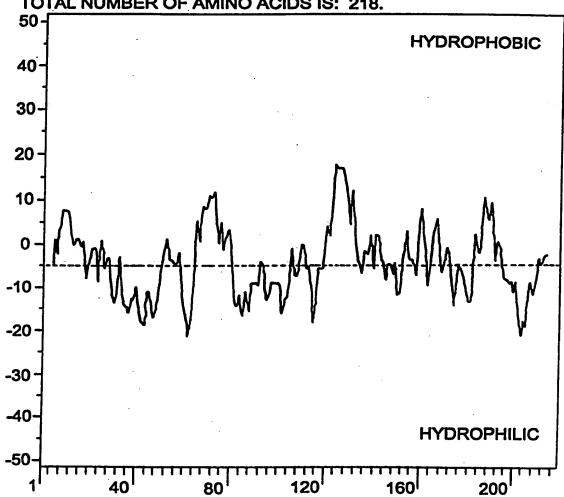






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HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPB. TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPB FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-4.95).

FIG. 3A.

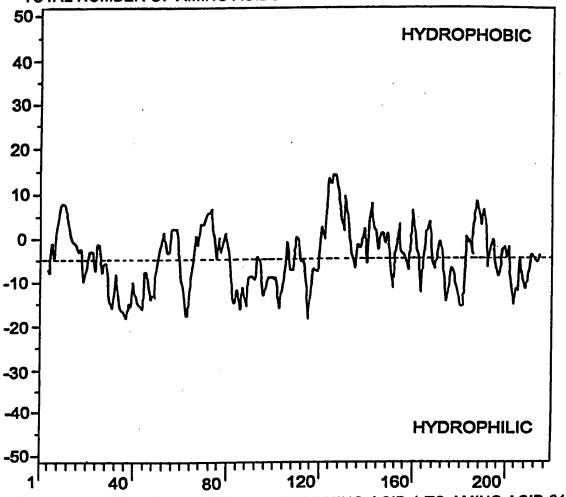


Involver(s): Rao et al. Application No: 09/478,598

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# HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM10. TOTAL NUMBER OF AMINO ACIDS IS: 218



HYDROPATHIC INDEX OF VSPM1 FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=5.52).

FIG. 3B.

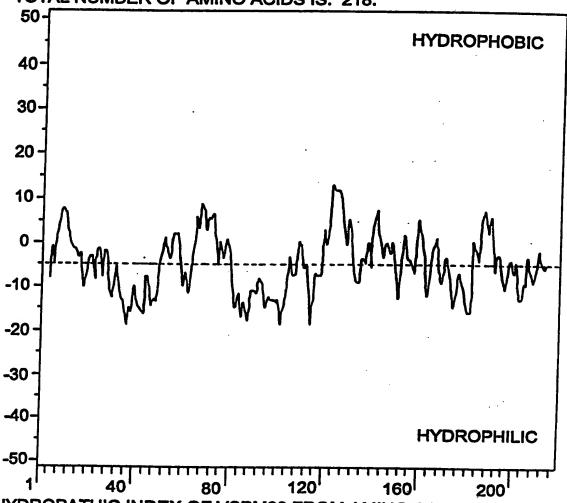
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Inventor(s): Rao et al. Application No: 09/478,598

Atty Dkt No: 5718-16A (35718/193734)

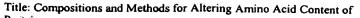






HYDROPATHIC INDEX OF VSPM20 FROM AMINO ACID 1 AMINO ACID 210. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.68).

FIG. 3C.



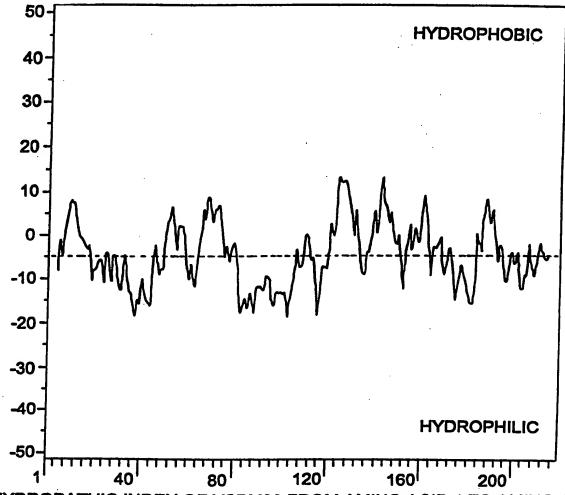


Investigation (s): Rao *et al.* Application No: 09/478,598

Atty Dkt No: 5718-16A (35718/193734)

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## HYDROPATHY INDEX COMPUTATION FOR SEQUENCE VSPM30. TOTAL NUMBER OF AMINO ACIDS IS: 218.



HYDROPATHIC INDEX OF VSPM30 FROM AMINO ACID 1 TO AMINO ACID 218. COMPUTED USING AN INTERVAL OF 9 AMINO ACIDS. (GRAVY=-5.31).

FIG. 3D.

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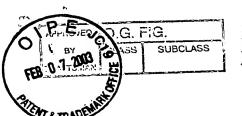


Inverse (s): Rao et al. Application No: 09/478,598 Atty Dkt No: 5718-16A (35718/193734)

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### VSPβ-met10 sequence

	<u>SfiI</u>	
1	GGCCAGCCGGCCAGATCTTCGGAGATGAAATGCGCTAGCTTTAGGCTTGCTGTGGAAGC	60
	CCGGGTCGGCCGGTCTAGAAGCCTCTACTTTACGCGATCGAAATCCGAACGACACCTTCG	
61	ACACAACATGCGAGCCTTTAAAACCATTCCTGAAGAGTGCATGGAACCAACAAAGGACTA	120
	TGTGTTGTACGCTCGGAAATTTTGGTAAGGACTTCTCACGTACCTTGGTTGTTTCCTGAT	
121	CATGAATGGCGAACAATTTCGAATGGACTCTAAAACAGTTAACCAACAGGCCTTCTTTTA	180
	GTACTTACCGCTTGTTAAAGCTTACCTGAGATTTTGTCAATTGGTTGTCCGGAAGAAAAT	
181	TGCTAGTGAAATGGAAATGCATCACAACGACATGTTTATATTCGGCATGGATAACACCAT	240
	ACGATCACTTTACCTTTACGTAGTGTTGCTGTACAAATATAAGCCGTACCTATTGTGGTA	
241	GCTCTCTAATATCCCATACTATGAAAAACATGGATATGGGGTGGAGGAATTTAATGAAAC	300
	CGAGAGATTATAGGGTATGATACTTTTTGTACCTATACCCCACCTCCTTAAATTACTTTG	
301	CTTATATGATGAATGGGTTAACAAGGGCGACGCACCGGCATTGCCAGAGACTCTTAAAAA	360
	GAATATACTACTTACCCAATTGTTCCCGCTGCGTGGCCGTAACGGTCTCTGAGAATTTTT	
361	TTACAACAAGCTGATGTCCCTTGGCTTCAAGATGGTATTCTTGTCAGGAAGGTACCTTGA	420
	AATGTTGTTCGACTACAGGGAACCGAAGTTCTACCATAAGAACAGTCCTTCCATGGAACT	
421	CAAAATGGCCGTAACAGAAGCAAACCTAATGAAGGCTGGCT	480
	GTTTTACCGGCATTGTCTTCGTTTGGATTACTTCCGACCGA	
481	<u>AATTCTCAAGGATCCACATCTTATGACTCCAAATGCACTTTCATACAAATCAGCAATGAG</u>	540
	TTAAGAGTTCCTAGGTGTAGAATACTGAGGTTTACGTGAAAGTATGTTTAGTCGTTACTC	
541	<u>AGAGAATATGTTGAGGCAGGGATACAGAATTGTTGGAATGATTGGTGATCAATGGAGCGA</u>	600
	TCTCTTATACAACTCCGTCCCTATGTCTTAACAACCTTACTAACCACTAGTTACCTCGCT	
601	TCTGCTTGGAGACCACATGGGCGAATCTAGAACCTTTAAGCTTCCTAATCCCATGTACTA	660
	AGACGAACCTCTGGTGTACCCGCTTAGATCTTGGAAATTCGAAGGATTAGGGTACATGAT	
661	CATGGAGGCGGCCGC 675	
	GTACCTCCGCCGGCG	
	Noti	



Title: Compositions and Methods for Altering Amino Acid Content of Propins In Dor(s): Rao et al.

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### COLONY LIFT ASSAY TO DETECT PROTEIN-PROTEIN INTERACTIONS

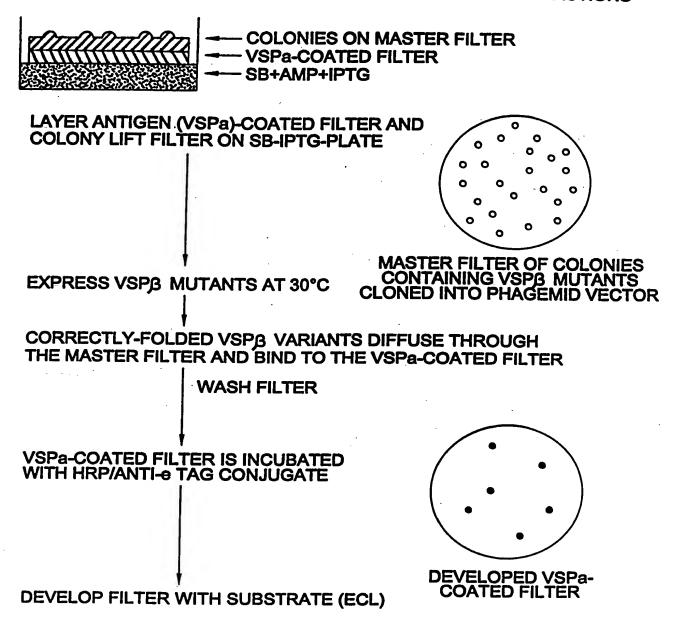


FIG. 5.